

CLAIMS

1. A PCR primer comprising a first sequence of a given base length which is complementary to one of single strands of target DNA and a second sequence
5 which is provided adjacent to the side of 5' terminus of said first sequence, has a GA or GC sequence at the side of 5' terminus and is non-complementary to the single strand of said target DNA.

2. A method for executing PCR amplification
10 comprising subjecting target DNA to PCR amplification with a first PCR primer which has a first sequence of a given base length complementary to one of single strands of target DNA, a GA or GG sequence at the side
15 of 5' terminus provided adjacent to the side of at 5' terminus of said first sequence, and a second sequence non-complementary to said target DNA, and a second PCR primer having a third sequence of a given base length complementary to the other single strands of said target DNA.

3. A PCR primer according to Claim 1, wherein
20 the base length of said first sequence is at 12 to 20.

4. A method for executing PCR amplification
according to Claim 2, wherein said second PCR primer or
25 both of said first and second primers are fluorescence labeled.

5. A method for analyzing a DNA fragment
comprising the steps of PCR amplification using a first PCR primer having a first sequence of a given base

length which is complementary to one of single strands of target DNA and a second sequence which has a GA or GG sequence at 5' terminus provided adjacent to the side of 5' terminus of said first sequence and a second
5 sequence non-complementary to said target DNA and a second PCR primer having a third sequence of a given base length which is complementary to one of other strands of said target DNA, and also using a
thermostable DNA polymerase having terminal transferase
10 activity, and detecting an amplified DNA fragment by electrophoresis.

6. A method for deciding a base sequence of a primer comprising providing four types of primers which, respectively, have a structure comprising a first
15 sequence of a given base length complementary to one of single strands of target DNA and a second sequence of a given base length non-complementary to said one single strand provided adjacent to the side of 5' terminus of said first sequence and which, respectively have, at 5'
20 terminus of said second sequence, one base whose types differ from one another, carrying out PCR by use of the four types of primers, analyzing the results of amplified products obtained by the PCR to obtain efficiencies of adenylation thereof, and deciding said
25 second sequence as a sequence which is most likely to undergo adenylation.

7. A method for deciding a base sequence of a primer according to Claim 6, which comprises selecting

one base at the 5' terminus of said second sequence,
providing four types of primers which, respectively,
have one base shifted from the 5' terminus by one base
toward the side of 3' terminus and individual bases
5 differ in type from one another, carrying out PCR by
use of the four types of primers, analyzing the results
of amplified products by the PCR to determine
efficiencies of adenylation, from which the one base
shifted from the 5' terminus by one base toward the 3'
10 terminus is decided, optionally further providing four
types of primers wherein the types of bases differ from
each other with respect to one base shifted further by
one base toward the 3' terminus and carrying out PCR the
last-mentioned four types of primers, analyzing the
15 results of amplified product by the last-mentioned PCR
to obtain efficiencies of adenylation, and successively
deciding said second sequence as one which is most
likely to undergo adenylation.

8. A method for deciding a base sequence of a
20 primer, which comprises providing four types of primers
which, respectively, have a structure comprising a
first sequence of a given base length complementary to
one of single strands of DNA and a second sequence of a
given base length non-complementary to said one single
25 strand provided adjacent to the side of 5' terminus of
said first sequence and which, respectively have, at 5'
terminus of said second sequence, one base whose types
differ from one another, carrying out PCR by use of the

four types of primers, analyzing the results of
amplified product obtained by the PCR to determine said
second sequence as a sequence that is most likely to
undergo adenylation whereby a second sequence that is
5 most likely to undergo adenylation is preliminarily
prepared, and checking, when target DNA is provided,
whether or not a primer composed of a combination of
the first sequence of a given base length complementary
to one of single strands of said target DNA and the
10 preliminarily prepared second sequence has a stable
secondary structure.

9. A service using the method defined in Claim 8,
wherein a base sequence which is likely to undergo
adenylation with and is non-complementary to given
15 target DNA is researched by use of the method of
deciding a base sequence of a primer recited in Claim 8,
designing a base sequence of a primer having the non-
complementary base sequence, and providing a base
sequence for said primer.

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